Flax belongs to the genus *Linum*, one of the ten genera in the family Linaceae. The genus encompasses more than hundred annual and perennial species. Cultivated flax pertains to the species, *Linum usitatissimum*, having two types: one is grown for oil (linseed) and the other for fibre (fibre flax). Textile properties of flax fibre are superlative to cotton. Flax is the third largest natural fibre crop and one of the five top oilseed crops in the World. It is a small size, self-pollinated herb that has been thought to be the best model fibre plant (Millam *et al.* 2005). Flax is commonly also known as, tisi, kshuma, lin, llion, liner, linum, line, linen, lein and lan. The plant is an annual which grows to a height of 110-120 cm and about 1.4-1.6 mm in diameter. In India flax is grown predominantly for linseed oil for human consumption and commercially it is utilized for paint, varnish, finished leather and printing ink. The history of flax dates back to 7000 BC when it was used by the Mesopotamians. Later on Egyptians, Babylonians, Greeks, Romans and other civilizations cultivated flax for its fibre. During the middle ages, linen was the most indispensable textile product. Hence flax is one of the antique and most interesting plants cultivated. The art of weaving flax was so advanced that wearing of ‘linen
cloth’ was considered to be a sign of aristocracy and gleaming whiteness of linen as a symbol of purity. In fact, the word ‘candidate’ used for office seekers has its origin from the Latin word ‘candidus’ which means white linen. The Egyptian art of weaving flax was gradually introduced in India, where linen was worn by many cases before the use of cotton. Presently as reported flax fibres producing countries are Belgium, Russia, Switzerland, Brazil, England, France and Argentina. The chief producer of flax fibre is the erstwhile Soviet Union, but the world’s best thread derives from Belgium and adjoining countries. In India the manufacturer of line fabrics, import the flax fibres from European countries and does not utilize the flax produced in India. The reasons for this are, Indian flax does not match with the quality standards of imported flax. But now several dual purpose varieties released are competent for both oil and fibre purpose. Among the oilseed crops, flax is next to rapeseed and mustard. India occupies 25% of world acreage and ranks first in the area (4.368 lac ha), fourth in production (1.725 lac tonnes) and eighth in productivity (395.0 Kg/ha) of the flax crop. The yield of fibre flax is about 10-15 quintal/ha. In India, small farmers grow linseed mainly for local consumption. This crop is not only commercially very important, but for the rural poor, it is a necessary means of survival. In spite of flax value as a food source, research directed toward the improvement of cultivated flax has been limited.

Therefore, germplasm characterization is an important link between the conservation and utilization of plant genetic resources. The diversity among varieties may be assessed based on morphological, biochemical and molecular markers. However, diversity analysis based on morphology alone has a significant limitation in the fact that the environment highly influences it. To overcome this problem, molecular characterization can play an important role. The development of molecular and biochemical techniques help researchers not only to identify genotypes but also in assessing and exploiting the genetic variability (Whitkus et al. 1994). However, systematic studies regarding the genetic diversity of flax through DUS descriptors as well as molecular markers in India are inadequate. Hence, in-depth studies based on morphological and molecular markers will help in understanding the genetic diversity of germplasm for the analysis of population structure, identification, conservation and utilization of authentic and superior crop materials.

**Crop History**

Flax or linseed is among the oldest crop plants cultivated for the purpose of oil and fibre for more than 6000 years, and it is among the first plants to be domesticated. The botanical name, *Linum usitatissimum* was given by Linnaeus in his book ‘Species Plantarum’ (Linnaeus, C. 1857). It was already cultivated in ancient Egypt and Samaria 10,000 years ago (Zohary and Hopf, 2000) to provide both fiber and oil. Recently, 30,000-year old processed and colored flax fiber was found, indicating that early humans made fabric or threads from the flax (Kvavadze et al. 2009). In ancient Egypt, linen was used for wrapping the royal mummies and additionally linseed oil was used to embalm the bodies of deceased Pharaohs (Dewilde, 1983).

In China and India domesticated flax was cultivated by at least 5,000 years ago (3,000 BCE). Portraits on tombs and temple walls at Thebes illustrate flowering flax plants. The use of flax fibre in the manufacturing of cloth in northern Europe dates back to Neolithic times. In Northern America, flax was first pioneered by the Puritans. For a long time flax has been cultivated as a dual-purpose crop, but now fibre flax and linseed represent different gene pools. Fibre flax has been cultivated in the Netherlands and most likely in Belgium and Northern France since ancient times. The quality and fineness of the linen have been proven ever since.

### Taxonomy and Nomenclature

<table>
<thead>
<tr>
<th>Scientific Classification</th>
<th>Kingdom</th>
<th>Division</th>
<th>Class</th>
<th>Order</th>
<th>Family</th>
<th>Genus</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Plantae</td>
<td>Magnoliophyta</td>
<td>Magnoliopsida</td>
<td>Malpighiales</td>
<td>Linaceae</td>
<td>Linum</td>
<td>L. usitatissimum</td>
</tr>
</tbody>
</table>

More than 200 species present in the genus *Linum* are distributed worldwide divided into five subsections (Tutin et al. 1968), of which subsection *Linum* contains the cultivated species *Linum usitatissimum* L. and the two ornamentals *L. grandiflorum* and *L. perenne*. *Linum* is the largest genus within the family and is found both in the Mediterranean region and the Americas. The two major user types are connected to morphotypes, broadly designed as oil (linseed; convar. mediterraneum), fiber (flax; convar. elongatum), and intermediate (convar. usitatissimum) varieties, although this infra-specific grouping is not unified (Diederichsen and Fu, 2006). The chromosome number of *Linum* species show a wide
range extending from $2n = 16$ to $2n = 72$ (Fedorov, 1974). *L. usitatissimum* and its wild relatives comprising $2n = 30$ chromosomes (Muravenko *et al.* 2003). The genome size (1C) of cultivated flax is 686 Mbp (Bennett and Leitch, 2004).

### Origin Distribution and Domestication

#### Centre of origin

The centre of origin of flax (*Linum usitatissimum* L.) is uncertain. It is considered that *L. bienne* as the progenitor of small seeded flax, originating from Kurdistan and Iran, whereas it is also sometimes considered that *L. angustifolium* containing high oil content and seed weight, as progenitor, originating from the Mediterranean region (Murre, 1955; Zeven and de Wet, 1975). Others suggest that *L. bienne* and *L. angustifolium* are the same species, and are widely distributed over Western Europe, the Mediterranean basin, North Africa, the Near East, Iran and Caucasus (Tutin *et al.* 1968; Zohary and Hopf, 1993). Contemporarily, a study with molecular markers advocated that the three species originated from one common ancestor, *L. angustifolium* being most primitive (Muravenko *et al.* 2003). *L. usitatissimum* is an annual crop species whereas, the wild forms can also be biennial or perennial. All species are predominantly self-pollinated (Zohary and Hopf, 1993). Cross pollination may occur (Williams, 1988) by artificial means through insects.

#### Domestication

Flax is indigenous to the region expanding from the eastern Mediterranean to India and was presumably first domesticated in the Fertile Crescent. It is cultivated throughout the world including Canada, India, China, United States, Ethiopia and all over Europe (FAOSTAT, 2013). Since the domestication of flax, there has been an inclination for growing flax either for its fibre or oil. In the Western region of Eurasia, flax is mostly grown for its fibre, whereas in the Eastern area of Eurasia flax is cultivated for its oil (Gill, 1987).

### Crop Botany

Flax cultivars are homogenous, and individual plants are considered homozygous (Anonymous, 1996). Flax is an annual plant growing 120 cm tall, with slender stems. The leaves are green, 20-40 mm long and 3 mm broad. The flowers are majorly pure pale blue and of various other colors, 15-25 mm diameter, with five petals. The fruit is a round, dry capsule 5-9 mm diameter, which may contain up to ten seeds when filled (Freeman, 1995). Seeds are glossy brown and 4-7 mm long. The kernels have a crisp and chewy texture and a pleasant, nutty taste (Carter, 1993). It is a herbaceous plant with shallow taproot system that may extend to a depth of 92-122 cm in the coarse textured soil.

### Growth Habit

The cultivars grown with intention to make fibre are tall growing with straight culms and have fewer secondary branches, and are conventionally grown in cool temperate regions of the world. The cultivars grown primarily for seed/oil purpose are relatively short in height and possess more secondary branches and seed bolls (seed capsule), and generally prefer the warmer climates such as those in the Mediterranean area, India, Canada and USA. Flax is mainly self-pollinated, but natural crossing is possible through insect. The frequency of cross-pollination seems to be related with varietal differences and environmental factors. In flax, individual flowers open in the first few hours after sunrise on clear, warm days, and the petals usually fall before noon. Most of the commercial varieties have blue petals. Petals may also be white or different shades of purple, blue or pink. The seeds are of various shades of yellow, brown, greenish-yellow, greenish-brown, or nearly black. Seed colour of most commercial varieties is light brown. Flax is an excellent companion crop to help establish small-seeded grasses and legumes. Plant characteristics that advocate its use as a companion crop are: (1) limited leaf area and short stature that allow enough light to reach the forage seedlings, (2) early maturity and (3) less extensive root system than many crops which reduces competition for soil moisture. Flax is an annual spring crop with 90 to the 110-day growing season. The typical life cycle consists of 45 to 60-day vegetative period, followed by a 15 to 25-day flowering period, and 30 to 40 day maturation period. Proper harvest time is critical in flax production. Early harvest diminishes yield while late harvest can change the chemical make-up of the oil and thus its quality and value.

### Agronomical Aspects

Fibre flax and linseed perform best in different regions. Fibre flax is mainly grown in climates with a relatively low temperature and high air humidity, which is characteristic for northern temperate regions. The subtropical regions and highlands are ideal locations for linseed cultivation, and, therefore, linseed should be more tolerant to prolonged periods of drought (Bunting, 1951). Although the soil type is not the most important
factor in flax cultivation, the sandy clay soils are very suitable for fibre flax cultivation. Flax requires a wide crop rotation of about seven years. Also, the preceding crop is important for growing flax to prevent the occurrence of diseases and lodging. As a rule of thumb, flax is sown at day 100 of the year and harvested on day 200, which is a growing period of 100 days. However, this depends somewhat on the cultivar and environmental conditions. The high sowing density of fibre flax of 110-130 kg/ha results in plant elongation due to the competition for light. It is important to obtain long, high-quality unbranched fibres. Linseed is sown with a lower density, 25-55 kg/ha (Rowland, 1998) to stimulate branching to obtain greater numbers of flowers and an increased seed yield. Flax starts to bloom approximately 11 to 14 weeks after sowing. The flowers are open for only a couple of hours in the morning, after which the petals fall off, and sepals close. Ten to 14 days after flowering the fruit reaches its final size, after which the weight remains stable until it decreases as a consequence of the ripening process. At the end of the development the flax plant hardens, turns to yellow (senescence) and loses its leaves. At a certain point, the plants are ready for the retting process, although the seeds might not be fully ripened. The retting process is the most crucial phase of flax cultivation because it determines the yield and quality of the fibre.

Importance
The flax is considered as one of the ancient and most utilitarian crops having separate utility. Cultivar development of flax for consumption is currently focused on augmenting the oil content and nutritional value to meet the requirement of nutraceutical market supply, as a substitute of fish oil, a rich source of eicosapentaenoic acid (EPA, C20:5) and docosahexaenoic acid (DHA, C22:6). Flaxseed is also rich in soluble and insoluble fibres and lignans, which makes it useful as a dietary supplement. Consumption of flaxseed in daily diet simplifies the risk of cardiovascular diseases such as coronary heart disease and stroke. There is also evidence that flax has anticancer effects in the breast, prostate and colon cancers. Flax fibre is used in the textile industry for making linen cloth and also in paper industry. The fibres of flax have great tensile strength, staple length, durability and fineness. They are used in the manufacture of linen cloth and thread, canvas, duck, strong twine, carpets, fish and seine lines, cigarette paper, writing paper and insulating materials. Fibres from the stalks of flax grown for seed are too harsh and brittle for spinning but may be used for other purposes. Some of the benefits of linen are that it is allergy-free, absorbs humidity and allows the skin to breathe, antistatic, antibacterial and low elasticity (fabrics don’t deform). Linen can be washed many times without alteration. It can absorb moisture up to 20 times its weight before it feels damp. The residues remaining after the oil extraction from linseed contains about 35-40% protein and 3-4% oil, a rich source of feed to livestock like cattle. Flax is naturally high in polyunsaturated fatty acids (PUFA), more specifically in ω-3 fatty acids; and hence flax seed as a component of poultry meal that can provide ω-3 enriched eggs. Rapid “drying” property of linseed oil is used for several purposes in industry, including paint and flooring (linoleum) industries. Due to its novel oil profile, flax may also be a suitable platform crop for the synthesis of exceptional industrial and nutraceutical products.

Area and Production
Linseed is an old world crop that was probably cultivated first in Southern Asia and Mediterranean region. There has been a general downward trend in area planted to linseed that began shortly after World War–II. During

<table>
<thead>
<tr>
<th>Sl No.</th>
<th>Country</th>
<th>Production (tonnes)</th>
<th>Sl No.</th>
<th>Country</th>
<th>Production (tonnes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>France</td>
<td>83100.00</td>
<td>1</td>
<td>Canada</td>
<td>71200.00</td>
</tr>
<tr>
<td>2</td>
<td>Belgium</td>
<td>67300.00</td>
<td>2</td>
<td>China Mainland</td>
<td>398800.00</td>
</tr>
<tr>
<td>3</td>
<td>Belarus</td>
<td>44925.00</td>
<td>3</td>
<td>Russian Federation</td>
<td>325756.00</td>
</tr>
<tr>
<td>4</td>
<td>Russian Federation</td>
<td>39039.00</td>
<td>4</td>
<td>Kazakhstan</td>
<td>295020.00</td>
</tr>
<tr>
<td>5</td>
<td>China</td>
<td>24356.00</td>
<td>5</td>
<td>India</td>
<td>147000.00</td>
</tr>
<tr>
<td>6</td>
<td>China Mainland</td>
<td>24056.00</td>
<td>6</td>
<td>Sweden</td>
<td>22900.00</td>
</tr>
<tr>
<td>7</td>
<td>United Kingdom</td>
<td>14000.00</td>
<td>7</td>
<td>Argentina</td>
<td>17070.00</td>
</tr>
<tr>
<td>8</td>
<td>Netherland</td>
<td>11237.00</td>
<td>8</td>
<td>France</td>
<td>16147.40</td>
</tr>
<tr>
<td>9</td>
<td>Egypt</td>
<td>8500.00</td>
<td>9</td>
<td>Brazil</td>
<td>9734.00</td>
</tr>
<tr>
<td>10</td>
<td>Italy and Chile</td>
<td>3000.00</td>
<td>10</td>
<td>Spain</td>
<td>8500.00</td>
</tr>
<tr>
<td></td>
<td>World + Total</td>
<td>303113.00</td>
<td></td>
<td>World + Total</td>
<td>2305369.07</td>
</tr>
</tbody>
</table>

Table 1: Top ten fibre flax and linseed producing countries in the World (FAOSTAT 2013)
2006, the total global linseed area was 3.02 million hectares with a production of 2.57 million tonnes and productivity of 852 kg/ha. According to FAOSTAT 2013, the total global production of fibre flax and linseed is given in Table 1.

In India, linseed is cultivated in about 4.68 lakh ha and the total linseed production is 1.63 lakh tonnes with 349 kg/ha productivity (2007-08). Madhya Pradesh, Uttar Pradesh, Chhattisgarh, Maharashtra, Bihar and Orissa are major linseed producing states in India. It is grown to a small extent in Jharkhand, Karnataka, Assam, Rajasthan, West Bengal, Himachal Pradesh, etc. There has been a continuous decline in linseed area in the country during last four decades. Linseed recorded annual compound growth rates of -2.11, -1.19 and 0.93% in area, production and productivity during 1950-51 and 2006-07. Presently in India linseed area harvested is about 4.31 lakh ha and production is 1.52 lakh tonnes.

These data are not available in case of fibre flax and tows for India. The total world area harvested for linseed is approx 2.34 million ha and for fibre flax and tows it is 2.18 lakh ha. (FAOSTAT 2012).

India imports fibre flax worth ₹150 crore approximately. Belgium is the largest supplier of fibre flax accounting for imports worth ₹104 crore followed by France and Netherlands, which export fibre flax worth ₹40 crore and ₹6 crores respectively. Kolkata Sea accounted for 78.9% of imports followed by Nhava Sheva Sea and Tuticorin Sea, which account for 9.7% and 8.4% of imports respectively (www.zauba.com).

Genetic Diversity and its Importance

Biodiversity can be defined at genetic, species and community levels of biological organization. Even though genetic diversity is in the lowest in the hierarchy, without genetic diversity, a population cannot

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**Table 2.** Details of different studies about the genetic diversity in flax using morphological characters

<table>
<thead>
<tr>
<th>Parameters /Characters studied</th>
<th>Material(s) used for study</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dimensional Parameters such as Length, Width, Thickness, Geometric mean diameter, Surface area and Aspt ratio.</td>
<td>Kernels of Twelve linseed varieties.</td>
<td>S. Sharma and K. Prasad, 2013</td>
</tr>
<tr>
<td>Plant height (PH); Days to flowering (DF); Days to maturity (DM); Primary branches per plant (PB/P); Secondary branches per plant (SB/P); Number of bolls per plant (B/P); Number of seeds per boll (S/B); Seed yield per plant (SY/PT); Seed yield per plot (SY/PT); Thousand seed weight (TSW) Oil content (Oil%) Oil yield per plot (Oil yield).</td>
<td>Sixty accessions of linseed, mainly from Ethiopia.</td>
<td>W. Adugna, M.T. Labuschagne and C.D. Viljoen, 2006</td>
</tr>
<tr>
<td>Eighteen morphological characters in a grow-out test (GOT).</td>
<td>Four flax cultivars (Kartika, Deepika, Indira Alsi 32 and RLC 92).</td>
<td>Palli et al. 2014</td>
</tr>
<tr>
<td>Straw yield/plant (g); Biological yield/plant (g); Seed yield/plant (g); No. capsules/plant; technical length (cm) and plant height (cm) and between biological yield/plant (g) with each of No. capsules/plant; length of the fruiting zone (cm); technical length (cm) and plant height (cm) and between seed yield/plant (g) with length of the fruiting zone (cm) and plant height (cm) and between No. capsules/plant with technical length (cm) and plant height (cm) and finally between both plant height (cm) and technical length (cm).</td>
<td>Six flax cultivars of diverse origins were grown during three successive seasons with three sowing dates in each growing season.</td>
<td>Ottai M.E.S et al. 2011</td>
</tr>
<tr>
<td>Seven quantitative traits measured on whole seeds and three quantitative traits measured on longitudinal seed section.</td>
<td>Six linseed genotypes from two harvested years – 2010 (5 genotypes), 2012 (5 genotypes).</td>
<td>Janka Nőzková et al. 2014</td>
</tr>
<tr>
<td>Sixteen quantitative charisms.</td>
<td>Twenty one parent flax genotypes and twenty F₂ hybrids.</td>
<td>IAA Kandil et al. 2012</td>
</tr>
<tr>
<td>Developed and used a set of morphological descriptors to determine levels and patterns of diversity in Ethiopian germplasm.</td>
<td>One hundred ninety eight Ethiopian traditional varieties.</td>
<td>Worklu et al. 2014</td>
</tr>
<tr>
<td>Morphological and seed-oil characters were used to describe the phenotypic diversity.</td>
<td>2331 flax accessions.</td>
<td>Diedrichschen, 2001</td>
</tr>
<tr>
<td>Investigated variation and relationships among seed colour, seed weight and seed oil content in cultivated flax (Linum usitatissimum L. ssp. usitatissimum).</td>
<td>2934 flax accessions from 72 countries for describe the variation of the seed characters.</td>
<td>Diedrichschen and Raney, 2006</td>
</tr>
</tbody>
</table>
metamorphose and adapt to environmental changes. The genetic diversity has an impact on the higher levels of biodiversity (Templeton, 1991, 1993). Genetic biodiversity discovers its natural resources in wild species for which it is necessary to reveal out the amount of genetic variability by the way of morphological, biochemical and molecular markers. Characterization of diversity has long been based on morphological traits mainly. However, morphological variability is often restricted, characters may not be visible at all stages of the plant development, and appearance may be affected by environment (Neilsen, 1985). Nowadays, a variety of different genetic markers has been proposed to assess genetic variability as a complementary strategy to more traditional approaches in genetic resources management (Sharopova et al. 2002; Hirata et al. 2006). Understanding the molecular basis of the essential biological phenomena in plants is crucial for the effective conservation, management, and efficient utilization of plant genetic resources (PGR). In particular, sufficient knowledge of existing genetic diversity, wherein a plant population it is found and how to best utilize it, is of paramount interest for basic science and applied aspects like the efficient management of crop genetic resources. The improvement of crop genetic resources is dependent on continuous infusions of wild relatives, traditional varieties and the use of modern breeding technologies. These processes require an assessment of diversity at some level, to select resistant, highly productive varieties.

**Genetic Diversity in Flax**

The availability and knowledge about the extent of genetic diversity of genetic resource material play a major role in identifying parental lines and developing new varieties with desirable traits. Morphological trait-based diversity assessment has been widely used in crop plants including linseed (Diederichsen, 2001; Diederichsen and Raney, 2006; Saeidi, 2008) (Table 2); however the morphological characters are not only sensitive to environmental factors but they also require labour intensive field evaluation over extended periods of time.

**Table 3.** List of Molecular markers developed in flax for the genetic diversity analysis

<table>
<thead>
<tr>
<th>Markers generated</th>
<th>Motif identified</th>
<th>Primer designed</th>
<th>Material used for study</th>
<th>Application of marker</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Expressed sequence tags (ESTs)</strong></td>
<td>Eighty three SSR motifs were identified.</td>
<td>662 primer pairs</td>
<td>23 flax accessions</td>
<td>Development of genetic and physical maps, quantitative trait loci mapping, genetic diversity studies, association mapping and fingerprinting cultivars.</td>
<td>Sylvie Cloutier et al. 2009</td>
</tr>
<tr>
<td><strong>Putative simple sequence repeats (SSRs)</strong></td>
<td>Out of 1,506 putative SSRs, 1,164 were derived from BAC-end sequences (BESs) and 342 from expressed sequence tags (ESTs). Trinucleotide = most abundant and Dinucleotide = most polymorphic.</td>
<td>673 (58 %) and 145 (42 %) primer pairs being polymorphic in the BESs and ESTs, respectively.</td>
<td>Panel of 16 flax accessions</td>
<td>Useful in genetic, quantitative trait loci (QTL) and association mapping as well as for anchoring the physical/genetic map with the whole genome shotgun reference sequence of flax.</td>
<td>Sylvie Cloutier et al. 2012</td>
</tr>
<tr>
<td><strong>SSR markers</strong></td>
<td>Contigs and the singlets contained 1,842 microsatellite motifs, with dinucleotide motifs as the most abundant repeat type (54%) followed by trinucleotide motifs (44%).</td>
<td>290 SSR markers were designed</td>
<td>Panel of 27 diverse linseed genotypes</td>
<td>Utility of next-generation sequencing technology for efficiently discovering a large number of microsatellite markers in non-model plants.</td>
<td>Sandip M. Kale et al. 2012</td>
</tr>
<tr>
<td><strong>Simple sequence repeats (SSRs)</strong></td>
<td>SSR sequences were isolated from the flax genome using a modified fast isolation by amplified fragment length polymorphism of sequences containing repeats (FIASCO procedure.</td>
<td>92 SSRs</td>
<td>12 flax varieties and seven related <em>Linum</em> species</td>
<td>Markers add to the resources available for genetic mapping and variety identification in flax.</td>
<td>Cory L Bickel et al. 2011</td>
</tr>
<tr>
<td><strong>Microsatellite markers</strong></td>
<td>38 SSR markers located across the 30 chromosomes of flax were used for fingerprinting the selected flax cultivars.</td>
<td>28 SSR markers</td>
<td>four flax cultivars (Kartika, Deepika, Indra Alsi 32 and RLC 92)</td>
<td>Practical utility of the SSR markers in assessing the genetic purity of the flax cultivars.</td>
<td>Palli et al. 2014</td>
</tr>
</tbody>
</table>
Table 4. Details of some major marker systems used for the genetic diversity analysis of flax reflecting the material studies

<table>
<thead>
<tr>
<th>Marker system</th>
<th>Primer/Isozyme details</th>
<th>Material(s) used for study</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AFLP</strong></td>
<td>Sixteen primer combinations: E-ACA/M-CAC; E-ACA/M-CAG; E-ACA/M-CAT; E-ACA/M-CTA; E-AAC/M-CAA; E-AAC/M-CAG; E-AAC/M-CAT; E-AAC/M-CTT; E-AGC/M-CAC; E-AGC/M-CAG; E-AGC/M-CAT; E-AGC/M-CTA; E-AGC/M-CTC E-AGC/M-CTT; E-AAGM-CAA; E-AGG/M-CAA</td>
<td>Characterized and evaluated the level of genetic diversity among some of the prominent (45) Indian genotypes of linseed.</td>
<td>Chandrawati et al. 2014</td>
</tr>
<tr>
<td><strong>RAPD</strong></td>
<td>Nine RAPD primers</td>
<td>Evaluated the genetic relationship among three ecotypes of flax.</td>
<td>T. H. S. Abou El-Nasr and Heba A. Mahfouze, 2013</td>
</tr>
<tr>
<td><strong>RAPD</strong></td>
<td>120 (RAPD) markers</td>
<td>Molecular characterization of 40 linseed varieties/genotypes.</td>
<td>Ambreen Ijaz et al. 2013</td>
</tr>
<tr>
<td><strong>AFLP</strong></td>
<td>Seven pairs of AFLP primers: M2, M3, M4, M5, M6, M7, M8</td>
<td>Genetic diversity of Sixty accessions of linseed.</td>
<td>Adugna Wakjira et al. 2005</td>
</tr>
<tr>
<td><strong>Inter-Retrotransposon Amplified Polymorphism (IRAP)</strong></td>
<td>10 IRAP primers: 1826, 1833, 1838, 1845, 1846, 1854, 1868, 1881, 1886, 1899</td>
<td>Evaluated genetic diversity among 708 accessions of cultivated flax comprising 143 landraces, 387 varieties, and 178 breeding lines.</td>
<td>P. Smykal et al. 2011</td>
</tr>
<tr>
<td><strong>ISSR and RAPD</strong></td>
<td>One ISSR primer (UBC 889) and two RAPD primers (UBC 556 and 561)</td>
<td>The microspore origin of anther-culture-derived 16 Flax plants.</td>
<td>Y. Chen et al. 1998</td>
</tr>
<tr>
<td><strong>RAPD</strong></td>
<td>Twenty-nine primers (UBC primers 220, 250, 301, 310, 335, 336, 337, 338, 365, 373, 388, 391, 396, 502, 526, 540, 542, 548, 556, 569, 574, 586, 711, 731, 737, 743, 775, 790, and 795)</td>
<td>Genetic diversity and relationships in 22 Canadian cultivars, 29 selected world cultivars and 10 landraces of flax</td>
<td>Yong-Bi Fu et al. 2002</td>
</tr>
<tr>
<td><strong>RAPD</strong></td>
<td>29 informative RAPD primers</td>
<td>Genetic diversity in 12 flax accessions representing seven flax species in the genus <em>Linum.</em></td>
<td>Yong-Bi Fu et al. 2002</td>
</tr>
<tr>
<td><strong>RAPD, ISSR, REMAP, SLP (simple length polymorphism) and IRAP markers</strong></td>
<td>A set of 10 RAPD and 15 ISSR primers</td>
<td>Genetic diversity in 18 flax accessions.</td>
<td>Jana Žiarovská et al. 2012</td>
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<tr>
<td><strong>ISSR</strong></td>
<td>Twelve ISSR primers</td>
<td>Seventy Indian flax genotype.</td>
<td>Rajwade et al. 2010</td>
</tr>
<tr>
<td><strong>RAPD</strong></td>
<td>54 North American flax cultivars.</td>
<td></td>
<td>Yong et al. 2004</td>
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<tr>
<td><strong>RAPD</strong></td>
<td>3101 accessions of cultivated flax (<em>Linum usitatissimum L. subsp. usitatissimum</em>).</td>
<td></td>
<td>Diederichsen and Yong, 2006</td>
</tr>
<tr>
<td><strong>AFLP</strong></td>
<td>Six AFLP primer combinations</td>
<td>Characterize a set of flax germplasm, along with one Turkish cultivar, one Russian cultivar, five winter and four dehiscence type accessions of cultivated flax.</td>
<td>Everaert et al. 2001</td>
</tr>
<tr>
<td><strong>ISSR</strong></td>
<td>Twenty-four ISSR primer</td>
<td></td>
<td>Hüseyin et al. 2010</td>
</tr>
<tr>
<td><strong>(EST-SSR) primer pairs</strong></td>
<td>49 informative expressed sequence tag-derived simple sequence repeat (EST-SSR) primer pairs.</td>
<td>Assess genetic relationships of 63 <em>Linum</em> accessions representing seven typical groups of cultivated flax and its wild progenitor, pale flax (<em>Linum bienne Mill.</em>).</td>
<td>Yong, 2011</td>
</tr>
</tbody>
</table>
On the other hand, DNA-based molecular markers have several advantages like abundance, environment independent early and rapid assessment and non-tissue specific characteristics. Oh et al. first reported the use of DNA-based markers to study flax diversity, (2000) who compared RAPD and RFLP techniques and generated a preliminary genomic map based on these marker data. Molecular characterization of flax germplasm has been made using various molecular techniques to assess genetic diversity of cultivated flax and to examine evolutionary relationships of wild flax species. High-quality seeds and elite cultivars play a crucial role in flax production.

However, since novel cultivars in general arise from hybridizations between members of an elite group of genetically alike parents, the amount of genetic instability among newly developed cultivars is likely to become even insignificant (Rahman et al. 2009), which makes it more tiresome to decipher ably distinguish cultivars from the others with morphological characteristics and biochemical markers because of influences by environmental factors (Table 2). Fingerprinting with molecular markers allows precise, objective and rapid cultivar identification, which has been proved to be an efficient tool for crop germplasm characterization, collection and management. Multipurpose uses with whole plant utilisation for several purposes including industrial food, animal feed, fibre, nutraceutical, pharmaceutical and bioproduct markets. Genetic diversity analysis of linseed germplasm can reveal the extent of genetic relatedness among accessions by estimating their genetic distance and is useful in the conservation of genetic resources. It is also necessary for cultivar identification and seed certification programmes.

Under the International Union for the Protection of New Varieties of Plants (UPOV, 1991), plant breeders’ rights (PBR) are based on criteria of distinctiveness, uniformity and stability (DUS) of genotypes. To identify potentially novel genotypes among the flax accessions, and to assess genetic diversity for both germplasm management and core collection (Frankel and Brown, 1984) assembly, molecular markers are highly useful. A variety of marker systems, including Random Amplified Polymorphic DNA (RAPD), Inter-Simple Sequence Repeat (ISSR), Amplified Fragment Length Polymorphism (AFLP) and simple sequence repeat (SSR) been used to analyze flax germplasm (Cloutier et al. 2009; Diederichsen and Fu, 2006; Everaert et al. 2001; Fu, 2002, 2005; Fu et al. 2002a, b, 2003; van Treuren et al. 2001; Wiesnerova and Wiesner, 2004) (Table 3 and Table 4). Taken together, these studies show that cultivated flax has low genetic diversity compare to wild relatives or some other crops (Smykal et al. 2008a), possibly resulting from a domestication bottleneck.

The details of molecular marker developed in flax have been given in Table 3. In apparent contradiction to the lack of diversity indicated by marker studies, the flax genome shows environmentally induced yet heritable genomic changes, a phenomenon of interest for many

<table>
<thead>
<tr>
<th>Marker system utilized</th>
<th>Population studied</th>
<th>Software used</th>
<th>Result</th>
<th>Reference</th>
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<tr>
<td>150 microsatellite loci</td>
<td>To assess the population structure, genetic diversity and LD of a set of 60 flax cultivars/ accessions capturing the breadth of SM (seed mucilage) variation in flax germplasm.</td>
<td>Structure</td>
<td>Collection could be useful in AM studies aimed at the discovery of genes/alleles involved in SM.</td>
<td>Soto-Cerda et al. 2013</td>
</tr>
<tr>
<td>448 microsatellite markers</td>
<td>407 globally distributed flax accessions</td>
<td>Structure</td>
<td>Core collection is suitable for AM studies targeting multiple agronomic and quality traits aiming at the improvement of flax as a true dual purpose crop.</td>
<td>Braulio J. Soto-Cerda et al. 2012</td>
</tr>
<tr>
<td>460 microsatellite markers</td>
<td>390 accessions</td>
<td>Structure</td>
<td>The candidate QTL identified herein will establish the foundation for future marker-assisted breeding in linseed.</td>
<td>Braulio J. Soto-Cerda et al. 2014</td>
</tr>
<tr>
<td>Agronomic traits</td>
<td>35 linseed genotypes</td>
<td>Structure</td>
<td>The combined application of the stability, AM and QQE analyses could accelerate the development of marketable linseed cultivars adapted to Southern Chile.</td>
<td>Braulio J. Soto-Cerda et al. 2014</td>
</tr>
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</table>
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Evans *et al.* (1966) observed that conventional breeding methods for this crop, which produce pure lines through successive generations of inbreeding, are time-consuming. Breeding flax using haploid techniques has the potential advantages of rapid development of completely homozygous lines within one generation and the development of efficient means of genotypic selection. Friedt *et al.* (1995) introduced anther culture as the most successful method for producing doubled haploid lines in flax. Given such recent development of linseed cultivars and the historical significance of flax cultivation, it is surprising to learn that few studies have been made to assess the genetic diversity of flax germplasm with molecular techniques. Analyses of the extent and distribution of genetic variation within and among various flax germplasms are essential for understanding genetic relationships among accessions, and for sampling genetic resources for breeding and conservation purposes (Ayad *et al.* 1997). The details about the molecular diversity of flax have been given in Table 4.

### Association Mapping Studies in Flax

Association mapping (AM) takes advantage of an extensive range of germplasm including natural populations and collections of varieties and breeding lines to map traits by linkage disequilibrium (LD), which is the non-random association of alleles at different loci (Myles *et al.* 2009). Parvaneh Asgarinia *et al.* (2013) conducted AM in flax to identify resistance QTL. The main advantage of AM is its high resolution in predicting the correlation between polymorphisms and QTL based on thousands of meiotic events accumulated during the shared history of the individuals in a population. Since *L. usitatissimum* has a long and complex domestication and different breeding history and considering its limited gene flow, it is expected that flaxseed populations exhibit complex population structures. Information on population structure has important implications because population structure is the primary source of spurious associations (Chao *et al.* 2010; Flint-Garcia *et al.* 2003). Therefore, population structure must be investigated to determine the potential for association analyses (Song *et al.* 2009). Moreover, assessing the genetic relatedness among the accessions of the targeted population is an essential prerequisite for the identification of nonredundant core collections suitable for optimizing LD estimation and association studies (Maccaferri *et al.* 2005).

### Conclusion

Assessment of genetic variability is the first step in any crop improvement programme. Diversity analysis is an essential process for precise and accurate identification of the genetic relatedness of the available genetic resources. It is also required for effective choice of parents for next crossing and selection of the progenies. Flax (*Linum usitatissimum subsp. usitatissimum*) is one of the founding crops with diverse importance. Since flax, and, in particular, fibre flax, has been such an important cultivated crop, it is of great significance to conserve as...
widely genetic material of flax as possible for future utilisation in breeding. To maintain and exploit these genetic resources efficiently, an understanding of the amount and distribution of genetic variation within and among accessions in a collection is required. Thus, study of the extent and distribution of genetic variation within and among various flax germplasms are essential for understanding genetic relationships among accessions, and for sampling genetic resource for breeding and conservation purposes. Further study research in this area shortly will facilitate germplasm management and enhance the utilization of germplasm in designing specific flax breeding programme.

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Dewilde, B., 1983. 20 eeuwen vlas in Vlaanderen: 439 PP.


Diederichsen, A. and Raney, J. P. 2006. Seed colour, seed weight and seed oil content in Linum usitatissimum accessions held by Plant Gene


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resource collections: a case study in flax using AFLPs. *Theor Appl Genet.* **103**: 144-152.


